

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	

Fig

Fig. 2

ICTB : 471	TGTCAGTGTCTACGGCTCAACCAATGGAICTACGGCGTTGAAGAGCTGGCGACTTGGGT	530
SLR : 483	GGTGGGAGTTACGGTCTGCGACAACAGGTGGACGGGTAGAACAGTTAGCCACTTGGAA	542
ICTB : 531	GGATCGCAACTCGGTTGCCGACTTCACCTCACGGGTTTACAGCTATCTGGGCAACCCCAA	590
SLR : 543	TGACCCCACTCTACCTTGGCCCCAGGCCACTAGGGTATATAGCTTTTAGGTAATCCCAA	602
ICTB : 591	CCTGCTGGCTGCTTAICTGTGTCGGACGACTGCCCTTTT-CTGCAGCAGCGATCGGGTGT	649
SLR : 603	TCTCTTGGCGGCTTACCTGTGTGCCCATGACGGGTTTGAGCTTGAGT-GCCCTGGTGGTAT	661
ICTB : 650	GGCGGGCTGGCTCCCAAGCTGCTGGCGATCG-CTGCGACAGGTGCGAGCAGCTTATGT	708
SLR : 662	GGCGACGGTGGTGCCCAAACTGCTGG-GAGCAACCATGGTGATTGTTAACCTACTCTGT	720
ICTB : 709	CTGATCCTCACCTACAGTCGGCGGTGGCTGGGTTTGTGCGCCATGATTTTGTCTGG	768
SLR : 721	CTCTTTTACCCAGAGCCGGGGCGGTTGGCTAGCAGTGTGCCCCCTGGGAGCTACCTTC	780
ICTB : 769	GGGTTATTAGGCTCTACTGTTTCAACCCCGTCTACCCGCACCCCTGGCGACGCTGGCTA	828
SLR : 781	CTGGCCCTTTGTTACTTCTGTTGTTACCCCAATTACCCAAATTTGGCAACGGTGGTCT	840
ICTB : 829	TTCCCAAGTCGTATTGGGTGGACTAGTCGGCGGTGCTCTT-GGTGGCGGTGCTTGGACT---	884
SLR : 841	TTGCCCTTGGC-----GATCGCC--GTGGCGGTTATATTAGTGGGGGAGCGTTGATTGGC	894
ICTB : 885	-TG-AGCCGTTGCGCGTGGCGGTGTTGAGCATCTTTGTGGGGCGTGAAGACAGCAACAAC	942
SLR : 895	GTGGAACCGATTTCGACTCAGGGCCCATGAGCATTTTGTGCTGGCGGGAAGACAGCAAGTAAT	954

Fig. 2
(Continued)

ICTB : 943 AACTTCGGGATCAATGCTCTGGCTGGCGGTGCTGCAGATGATTCAAGATCGGCCCTTGGCTG 1002
 SLR : 955 AATTTCGGCATCAATGTTTGGNAGGGGTAAAGCCATGATCCGAGCCCGCCCTATCATTT 1014

ICTB : 1003 GGCATCGGCCCGGCAATACCGCCTTTAACTGGTTTATCCCTCTATCAACAGCGCGC 1062
 SLR : 1015 GGCATTGGCCCGGCAAGGTTAAGAGCCTTTAACCAAAATTTATCTTACTATATCGGCCCGCC 1074

ICTB : 1063 TTTACGGCGTTGAGCGCCCTACTCCGTCGCCGCTGGAAGTCGCGGTTGAGGGCGGACTACTG 1122
 SLR : 1075 TTCACCGCCCTGAGTGCCTATTCCATTACCTAGAAATTTTGGTGAACGGGTGTAGTT 1134

ICTB : 1123 GGCTTGA-CGGCCTTCGCTTGGCTGCT-GCTGGTCACGGCGGTGACGGCGGTGCGGCAGG 1180
 SLR : 1135 GGTTTACCTGTATGCTC-TGGCTGTTGGCCGTTACCCCTAGGCAAGGC-GTAGAACTGG 1192

ICTB : 1181 TGAGCCGACTGCGGCGCGATCGCAATCCCC--ARGCCTTTTGGTTGATGGCTAGCTTGGC 1238
 SLR : 1193 TTAAACG-CTGTGCG-CRAACCCCTGCCCCCGGAAGGCATCTGGATTATGGGGCCTTTAGC 1250

ICTB : 1239 CGGTTTGGCAGGAATGCTGGGTACGGTCTGTTTGATACCGTGCTCTATCGACCGGAAGC 1298
 SLR : 1251 GCGCATCATCGGTTTGTGGTCCACGGCATGGTAGATACAGTCTGCTACCCCTCCCCCGGT 1310

ICTB : 1299 CAGTACGCTCTGGTGGCTCTGTATTGG--AGCGATCGCGAGTTTCTGG--CAGC-CCCAA 1353
 SLR : 1311 GAGCACCTTTGTGGTGG-TTGCTAGTGGCCATTG-TTGCTAGTCACTGGGCCAGCGGCCAG 1368

ICTB : 1354 CCTTCCAAGCAACTCCCTCCAGAAGCCGAGCATTTCAGACGAA 1395
 SLR : 1369 GCCCGTTTGGAGGCCCAGTAAAGAA---GAANATGAGGACAAA 1407

Fig. 2
(Continued)

+++W++L F + PQ+WG S LHRL G ++W +S L EALG L+A+++ +APF
 SLR : 5 ISIWRSIMFGGFPQEWGRGSLHRLVWGQSWIQASVLPHPHFEALGTALVAIIFIAAPF 64

ICTB : 61 VPSSALGLGLAAIAAYWALLSLTDIDLROATPIHVLVLLYWGVDALATGLSPVRAAALVG 120
 ++ LG+ + A+WALL+ D + TPIH LV YH + A+A G SPV+ AA G

SLR : 65 TSTTMLGIFMLLCCAFWALLTFADQPGKGLTPIHVLVFAIYWCISAIAGFSPVKMAASG 124

ICTB : 121 LAKLTLYLLVFALAAARVLRNPRLSLFSVVVITSLFVSVYGLNQWYGVVEELATWVDN 180
 LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + GVE+LATW D

SLR : 125 LAKLTANLCLFLLAARLLQNKQWLNRLVTVLLVGLLVGSYGLRQQVDGVEQLATWNDPT 184

ICTB : 181 SVADFTSRVYSYLGPNPMLLAAYLVPTTAFSAAGVWRGWLPKLLAIAATGASSLCLILT 240
 S +RVYS+LGNPNMLLAAYLVP T S +A+ VWR W PKLL + LCL T

SLR : 185 STLAQATRVYSFLGNPNMLLAAYLVPMTGLSLSALVVWRRWPKLLGATMVIVNLLCLFFT 244

ICTB : 241 YSRGGWLGFBAMIFVWALLGLYWFQPRLPAPZWRRLFPVVVLGGLVAVLLVAVLGLPLRV 300
 SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+

SLR : 245 QSRGGWLAVLALGATFLALCYFWWLPQLPKFWQWMSLPLAIAVAVILGGGALIAVEPIRL 304

ICTB : 301 RVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWLIGPGNTAFNLVPLYQQARFTALSA 360
 R +SIF GREDSSNNFRINVW V MI+ RP +GIGPGN AFN +YP Y + RFTALSA

SLR : 305 RAMSIFAGREDSSNNFRINVWEGVKAMIRARPIIGICPGNEAFNQIYPYMRPRFTALSA 364

ICTB : 361 YSVPLEVAVEGGLGLTAPAWLLLVTAVTAVRQVSRRLRRDRNPQAFWLMASLAGLMLG 420
 YS+ LE+ VE G++G T WLL VT V V R R+ P+ W+M +LA + G+L

SLR : 365 YSIYLBILVETGVVGFTCMWLLAVTLGKGVVELVKRCRQTLAPEGIMMGALAAIIGLLV 424

ICTB : 421 HGLFDTVLYRPEASTLWMLCIGAIASFWQPQPSKQLPPEAEHSDEKM 467
 HG+ DTV YRP STLWML + +AS W ++ + E+ D+ +

SLR : 425 HGMVDTVWYRPPVSTLWMLLVVAIVASQWASQAARLEASKEENEDKPL 471

Fig. 3

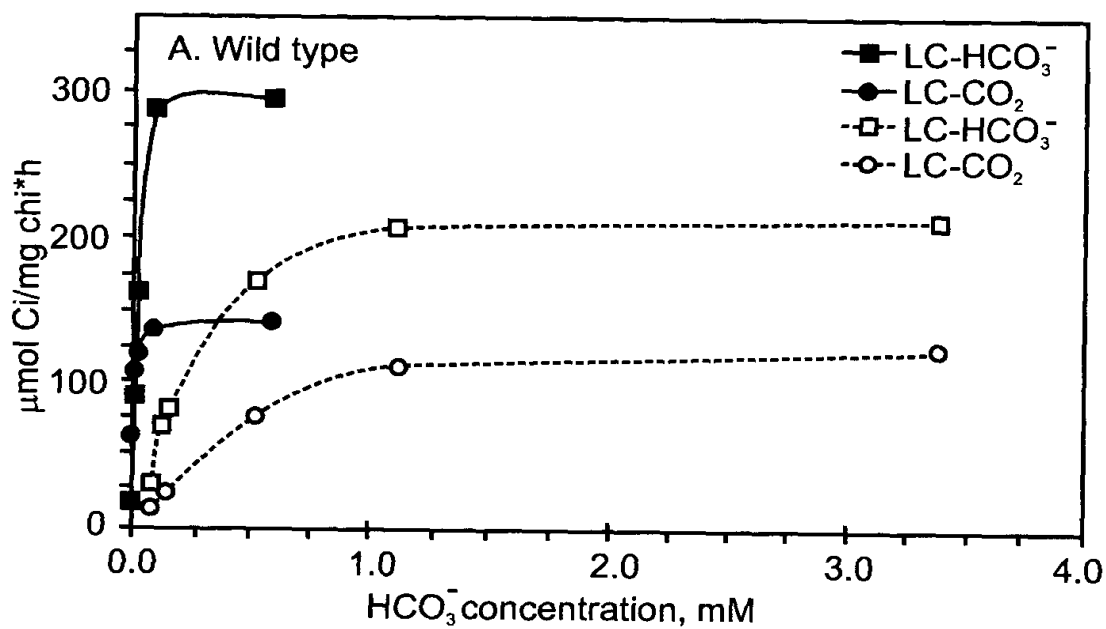


Fig. 4a

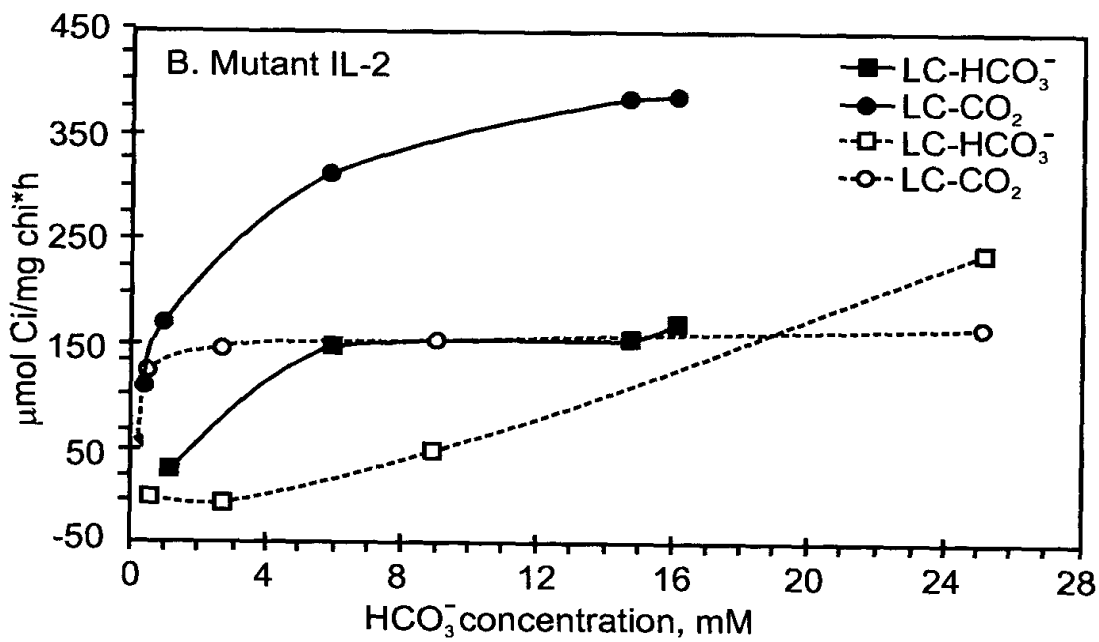


Fig. 4b

Wild type	GGGCT-AGCCGCCGATCGCGGCTATTGGGCC	(SEQ ID NO:6)
IL-2 ApaI side	GGGCT-AG--G-GATCGC-GCCTATTGGGCC	(SEQ ID NO:7)
IL-2 BamHI side	GGGCTCA-----GATCGC-GCCTATTGGGCC	(SEQ ID NO:8)
IctB	G L A A I A A Y W A L	(SEQ ID NO:9)

Fig. 5

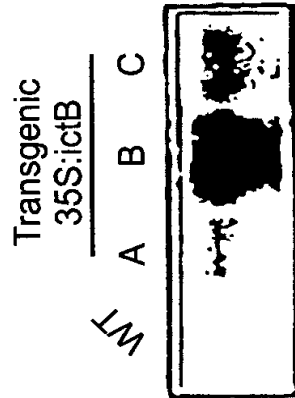


Fig. 6